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UniProtKB/Swiss-Prot entry Q69ZS6

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Entry information

Entry name	SV2C_MOUSE
Primary accession number	Q69ZS6
Secondary accession numbers	None
Integrated into Swiss-Prot on	June 13, 2006
Sequence was last modified on	June 13, 2006 (Sequence version 2)
Annotations were last modified on	June 10, 2008 (Entry version 32)
Name and origin of the protein	
Protein name	Synaptic vesicle glycoprotein 2C
Synonym	Synaptic vesicle protein 2C
Gene name	Name: Sv2c Synonyms: Kiaa1054
From	Mus musculus (Mouse) [TaxID: 10090]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Gli; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mice; 1: Evidence at protein level;
Protein existence	
References	[1] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]. TISSUE=Fetal brain; DOI=10.1093/dnarecs/11.3.205; PubMed=15368895 [NCBI, ExPASy, EBI, Israel, Japan] Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H., Nagase T., Ohara O., Koga H.;

"Prediction of the coding sequences of mouse homologues of KIAA gene: IV. The complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries."; DNA Res. 11:205-218(2004).

[2] INDUCTION.

DOI=10.1038/35087000; PubMed=11483953 [NCBI, ExPASy, EBI, Israel, Japan]
 Xu T., Bajjaleh S.M.;
 "SV2 modulates the size of the readily releasable pool of secretory vesicles.";
 Nat. Cell Biol. 3:691-698(2001).

[3] TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.

DOI=10.1002/cne.10636; PubMed=12687700 [NCBI, ExPASy, EBI, Israel, Japan]
 Wang M.M., Janz R., Belizaire R., Frishman L.J., Sherry D.M.;
 "Differential distribution and developmental expression of synaptic vesicle protein 2 isoforms in the mouse retina.";
 J. Comp. Neurol. 460:106-122(2003).

[4] FUNCTION AS A BOTA RECEPTOR.

DOI=10.1016/j.febslet.2006.02.074; PubMed=16545378 [NCBI, ExPASy, EBI, Israel, Japan]
 Mahrhold S., Rummel A., Bigalke H., Davletov B., Binz T.;
 "The synaptic vesicle protein 2C mediates the uptake of botulinum neurotoxin A into peripheral nerves.";
 FEBS Lett. 580:2011-2014(2006).

[5] FUNCTION AS A BOTA RECEPTOR.

DOI=10.1126/science.1123654; PubMed=16543415 [NCBI, ExPASy, EBI, Israel, Japan]
 Dong M., Yeh F., Tepp W.H., Dean C., Johnson E.A., Janz R., Chapman E.R.;
 "SV2 is the protein receptor for botulinum neurotoxin A.";
 Science 312:592-596(2006).

Comments

- **FUNCTION:** Plays a role in the control of regulated secretion in neural and endocrine cells by enhancing selectively low-frequency neurotransmission. Positively regulates vesicle fusion maintaining the readily releasable pool of secretory vesicles (*By similarity*).
- **FUNCTION:** Receptor for the botulinum neurotoxin type A/BOTA.
- **SUBUNIT:** Interacts with SYT1 in a calcium-dependent manner (*By similarity*).
- **SUBCELLULAR LOCATION:** Cytoplasmic vesicle, secretory vesicle, synaptic vesicle membrane; Multi-pass membrane protein (*By similarity*). Note=Enriched in small synaptic vesicles and adrenal microsomes, not present in chromaffin granules. Associated with insulin granules and synaptic-like microvesicles in insulin-secreting cells of the pancreas (*By similarity*).
- **TISSUE SPECIFICITY:** Expressed in specific subsets of conventional synapses in the retina (at protein level).
- **DEVELOPMENTAL STAGE:** Expressed during synaptogenesis in the retina (at protein level).
- **INDUCTION:** Up-regulated upon Sv2a depletion.
- **PTM:** N-glycosylated (*By similarity*).
- **SIMILARITY:** Belongs to the major facilitator superfamily.

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Cross-references**Sequence databases**

EMBL AK173092; BAD32370.1; ALT_INIT;
mRNA. [EMBL / GenBank / DDBJ]
[CoCodingSequence]

RefSeq XP_996351.1; -.

UniGene Mm.441155

3D structure databases

ModBase Q69ZS6.

Organism-specific databases

MGI MGI:1922459; Sv2c.

GeneLynx Sv2c; Mus musculus.

Gene expression databases

ArrayExpress Q69ZS6; -.

CleanEx MM_SV2C; -.

GermOnline ENSMUSG00000051111; Mus musculus.

Ontologies

GO GO:0008021; Cellular component: synaptic vesicle (*inferred from direct assay MGI*).

GO GO:0007268; Biological process: synaptic transmission (*traceable author statement from MGI*).

QuickGo

view.

Family and domain databases

IPR007114; MFS.

InterPro IPR011701; MFS_1.
IPR005988; SV2.

Graphical view of domain structure.

PANTHER PTHR11600:SF32; SV2; 1.

PF07690; MFS_1; 1.

Pfam Pfam graphical view of domain structure.

TIGRFAMs TIGR01299; synapt_SV2; 1.

PS50850; MFS; 1.

PROSITE PROSITE graphical view of domain structure (profiles).

BLOCKS Q69ZS6.

Genome annotation databases

Ensembl ENSMUSG00000051111; Mus musculus. [Contig view]

GenelD 75209; -.

NMPDR figJ10090.3.peg.28276; -.

Phylogenomic databases

HOVERGEN Q69ZS6; -.

Other

SOURCE Sv2c; Mus musculus.

ROUGE KIAA1054.

ProtoNet Q69ZS6.

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Cell junction; Cytoplasmic vesicle; Glycoprotein; Membrane; Neurotransmitter transpc Receptor; Synapse; Transmembrane; Transport.

Features



Feature table viewer



Feature aligner

Key	From	To	Length	Description	FTId
CHAIN	1	727	727	Synaptic vesicle glycoprotein 2C.	PRO_000023977
TOPO_DOM	1	154	154	Cytoplasmic (Potential).	
TRANSMEM	155	175	21	Potential.	
TOPO_DOM	176	191	16	Extracellular (Potential).	
TRANSMEM	192	212	21	Potential.	
TOPO_DOM	213	226	14	Cytoplasmic (Potential).	
TRANSMEM	227	247	21	Potential.	
TOPO_DOM	248	248	1	Extracellular (Potential).	
TRANSMEM	249	269	21	Potential.	
TOPO_DOM	270	280	11	Cytoplasmic (Potential).	
TRANSMEM	281	301	21	Potential.	
TOPO_DOM	302	320	19	Extracellular (Potential).	
TRANSMEM	321	341	21	Potential.	
TOPO_DOM	342	437	96	Cytoplasmic (Potential).	
TRANSMEM	438	458	21	Potential.	
TOPO_DOM	459	578	120	Extracellular (Potential).	
TRANSMEM	579	599	21	Potential.	
TOPO_DOM	600	609	10	Cytoplasmic (Potential).	
TRANSMEM	610	630	21	Potential.	
TOPO_DOM	631	636	6	Extracellular (Potential).	
TRANSMEM	637	657	21	Potential.	
TOPO_DOM	658	670	13	Cytoplasmic (Potential).	
TRANSMEM	671	693	23	Potential.	
TOPO_DOM	694	697	4	Extracellular (Potential).	
TRANSMEM	698	716	19	Potential.	
TOPO_DOM	717	727	11	Cytoplasmic (Potential).	
REGION	1	57	57	Interaction with SYT1 (By similarity).	
REGION	529	566	38	BOTB-binding (By similarity).	
CARBOHYD	480	480	0	N-linked (GlcNAc...) (Potential).	
CARBOHYD	484	484	0	N-linked (GlcNAc...) (Potential).	
CARBOHYD	534	534	0	N-linked (GlcNAc...) (Potential).	
CARBOHYD	559	559	0	N-linked (GlcNAc...) (Potential).	
CARBOHYD	565	565	0	N-linked (GlcNAc...) (Potential).	

Sequence information

Length: 727 AA [This is the Molecular weight: 82291 Da]

length of the unprocessed precursor]	[This is the MW of the unprocessed precursor]	CRC64: E1D78203D4E3183A is a checksum on the sequence
10	20	30
MEDSYKDRTS	LMKGAKDIAK	EVKKQTVKKV
40	50	60
	NQAVDRAQDE	YTQRYSYSRFQ
70	80	90
PGETYSGEVN	DDEGSSEATE	GHDEEDEIYE
100	110	120
	GEYQGIPSTN	QGKDSIVSVG
130	140	150
RELESERRAD	EEELAQGYEL	IIQECGHGRF
160	170	180
TDLCIPNSGS	GWLGSIVYLG	MMVGAFFWGG
190	200	210
	LADKVGRKQS	QWALFFVLGM
220	230	240
250	260	270
YGFFFLVCRLL	SGFGIGGAIP	TVFSYFAEVL
280	290	300
AREKRGEHLS	WLCMFWMIGG	IYASAMAWAI
310	320	330
IPHYGWSFSM	GSAYQFHCSR	VVFIVCALPC
340	350	360
	VSSVVALTFM	PESPRFLLEV
370	380	390
KLIHDTNMRA	RGQPEKVFV	NKIKTPKQID
400	410	420
ELIEIESDTG	TWYRRCFVRI	RTELYGIWLT
430	440	450
FMRCFNYPVR	ENTIKLTIVW	FTLSFGYYGL
460	470	480
SVWFPDVVIKH	LQSDEYALLT	RNVQKDKYAN
490	500	510
FSINFTMENQ	IHTGMNEYENG	RFLGVKFKSV
520	530	540
TFKDSVFKSC	TFDDVTSVNT	YFKNCTFIDT
550	560	570
LFDNTDFEPY	KFIDSEFQNC	SFLHNKTGCQ
580	590	600
ITFDDDSAY	WIYFVNFLGT	LAVLPGNIVS
610	620	630
ALLMDRIGRL	TMLGGSMVLS	GISCFFLWFG
640	650	660
TSESMMIGML	CLYNGLTISA	WNSLDVVTV
670	680	690
LYPTDERRATG	FGFLNALCKA	AAVLGNLIFG
700	710	720
SLVSITKAIP	ILLASTVLVC	GGLVGLRLPD
750	760	770
TRTQVLM		

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 BLAST ExPASy/SIB
or at NCBI (USA)



ProtScale, Compute pI/Mw, PeptideMass,
PeptideCutter, Dotlet (Java)



ScanProsite, MotifScan



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analysis tools

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